mechanism involved in X chromosome transcription, but the regulation of other two process is still obscure. The present investigation have been undertaken to explore the regulatory mechanism involved in X chromosome replication.

In our present study, different X chromosomal segmental aneuploids and hyperploids (see Stewart & Merriam 1975; Maroni & Lucchesi 1980) were constructed from different X;Y translocation stocks (T(X;Y) B44, J8 and B 29, Stewart & Merriam 1975). Metafemales (3X;2A) were produced by crossing attached-X females (C(I)RM, y pn/Y) to wild type males. Replication pattern of the salivary gland chromosomes were studied after pulse labelling with $^3\text{H-thymidine}$ (specific activity: 17,400 $_{\mbox{\sc l}}$ Ci/mM, BARC, Trombay, India; cons. 500 $_{\mbox{\sc l}}$ Ci/ml, exposure time 20 days).

Our results reveal that in individuals with 1.50 and 1.62 X chromosomal segments, each part of X chromosome (regardless haplo or diplo) is puffy, pale stained and early replicating (Fig. 1a). On the other hand, in all the aneuploid and hyperploids (from 1.85 to 2.85 X chromosomal segments), each part of X chromosome (regardless haplo, diplo or triplo) is narrower, intensely stained and exhibits synchronous pattern of replication with the autosomes (Fig. 1b). Interestingly, in metafemales (3X;2A), where per gene transcriptive activity is even lower than that of their diploid sisters (Lucchesi et al. 1974), individual (haplo) X chromosome is equal in diameter with that of individual (haplo) autosome and the X chromosome always replicate synchronously with the autosomes (Fig. 1c). Therefore, from all the above results, we would like to propose: (1) X chromosomal replication pattern, like transcription, does not depend upon X/A ratio, and (2) X chromosomal replication pattern always depend upon the relative diameter of the individual X chromosome, i.e., condensation or decondensation of X chromatin materials.

<u>Duttagupta</u>, A. and I.Roy. University of Calcutta, India. Isolation of nascent DNA from polytene chromosomes of Drosophila melanogaster.

The polytene chromosomes of Diptera offer a possibility to reveal whether ³H-TdR labelling pattern of the chromosome could be correlated with the size of the replication unit (Lonn 1980). The aim of the work presented here was to investigate whether nascent DNA fragments

can be selectively released from polytene chromosomes during cell lysis. If so, the size of the nascent DNA could give some insight into what particular replication pattern may be mean at the replicon level.

Third instar larvae of Drosophila melanogaster (giant) were used as the experimental material. Salivary glands were labelled with 3H-thymidine (77.2 Ci/m mole) for four hours and then transferred to a neutral non-denaturing lytic buffer. After 12 hours in lytic buffer at 20°C the lysate was transferred directly on to a polyacrylamide gel (5% concentration). The gel was run at 20 volts for four hours at room temperature and then stained with ethidium bromide. On visualization with a U.V. lamp a single band 6 mm from the top of the gel well was observed. The gel was sliced into 3 mm pieces and each piece was subjected to elution buffer individually, overnight in a 37°C water bath. The DNA was precipitated out with ethanol and lyophilized. Scintillation fluid (4% omniflouer in toluene) was added and the count taken on a Packard Scintillation Counter.

On taking the count two distinct peaks (Table 1) were obtained, with none in between. The first peak corresponded to the band visualized with U.V. The second peak corresponded to a position, right at the bottom of the gel, slightly smaller than the first one.

Table 1. Results of scintillation count of DNA isolated from the larval salivary gland of giant Drosophila melanogaster.

POSITIVE ID	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
TIME (min.)	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
GREEN CPM	52	63	175	108	44	37	49	51	44	52	63	37	23	72	140

Since lysis has been carried out in a neutral non-denaturing buffer and great care has been taken to avoid artefactural shearing, we have good reason to believe that the second peak corresponds to nascent DNA.

Reference: Lönn, U. 1980, Chromosoma 77:29-40.

Eggleston, P. University of Liverpool, Great Britain. Correlation in the induction and response of SF and GD sterility.

The occurrence of specific genetic aberrations in the progeny of certain outcrosses in Drosophila melanogaster is well documented. The abnormalities, which include reduced egg hatchability (SF sterility) and reduced egg

production (GD sterility) have been referred to collectively as "hybrid dysgenesis." It has been argued that two independent interactive systems contribute to the hybrid dysgenesis syndrome (Kidwell 1979). These are the I-R system (usually detected by the presence of SF sterility) and the P-M system (usually detected by the presence of GD

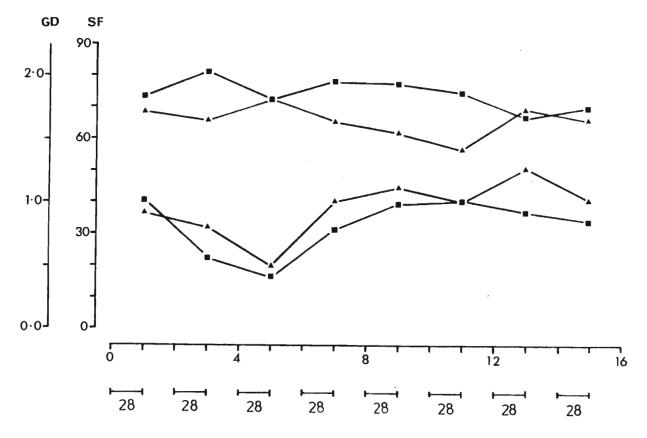


Fig. 1. Mean percentage egg hatchability or SF score () transformed to angles and mean egg production or GD score () transformed to square roots of the number of eggs laid per female per hour for both Cross A and Cross B. The x-axis shows developmental age at 18°C and the onset and duration of the 28°C pulse treatments is indicated by the black bars.